Identification of hydatid cyst genotypes in Qazvin

Abstract

Background: Hydatidosis is a serious parasitic disease in humans and livestock, worldwide. *Echinococcus granulosus* shows notable genetic variation among intermediate hosts. Several genotypes of the worm have been reported from different parts of Iran, but no information over the parasite genotypes status in the study region is available. The current study investigated the presence of different genotypes of *E. granulosus* in the livestock of Qazvin, Iran, by sequencing the mitochondrial cox1 genes.

Methods: Fifty *E. granulosus* isolates from sheep was collected from the slaughterhouses in Qazvin province. Mitochondrial cox1 gene region was amplified by PCR and 15 isolates were sequenced. Phylogenetic analysis was done by using the MEGA 7.0 software. Morphological analysis was performed on rostellar hook length of protoscoleces.

Results: All isolates were identified as *E. granulosus sensu stricto*. The Prevalence rate of G1 and G3 genotypes were determined 86.7% and 13.3% respectively. No significant difference between the rostellar hooks measurements of different genotypes was observed. The sequences were deposited in the GenBank database under the Accession Nos. MK5667-MK625679 و MK625663,MK625664.

Conclusion: The genotype of G1 was the predominant genotype among the specimens. Our findings confirmed the presence of a sheep-dog cycle in the region although further studies are required to determine the haplotype diversity of *E. granulosus* in the region.

Keywords: *Echinococcus granulosus,* Cox1, Genotype, Qazvin